

P. PONNALI

OIPE

RAW SEQUENCE LISTING

DATE: 09/07/2001

PATENT APPLICATION: US/09/486,882

TIME: 16:53:59

Input Set : N:\Crf3\08132001\I486882.raw

Output Set: N:\CRF3\09072001\I486882.raw

1 <110> APPLICANT: Rowett Research Institute Services limited
 2 <120> TITLE OF INVENTION: Chimeric binding peptide library screening method
 3 <130> FILE REFERENCE: P22410-/scr/bou
 4 <140> CURRENT APPLICATION NUMBER: US/09/486,882
 C--> 5 <141> CURRENT FILING DATE: 2000-02-03
 6 <160> NUMBER OF SEQ ID NOS: 78
 7 <170> SOFTWARE: PatentIn Ver. 2.0
 9 <210> SEQ ID NO: 1
 10 <211> LENGTH: 521
 11 <212> TYPE: DNA
 12 <213> ORGANISM: Recombinant human oestrogen
 13 <220> FEATURE:
 14 <221> NAME/KEY: CDS
 15 <222> LOCATION: (41)..(475)
 16 <400> SEQUENCE: 1
 17 aagcttgcac gcaaattcta tttcaaggag acagtcataa atg aaa tac cta ttg 55
 18 Met Lys Tyr Leu Leu
 19 1 5
 20 cct acg gca gcc gct gga ttg tta tta ctc gcg gcc cag ccg gcc atg 103
 21 Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met
 22 10 15 20
 23 gcc caa gtg cag ctg cag taa tag gcg gcc gca ggg gga gga ggg tcc 151
 24 Ala Gln Val Gln Leu Gln Ala Ala Ala Gly Gly Gly Gly Ser
 W--> 25 25 30 35
 26 atg gaa tct gcc aag gag act cgc tac tgt gca gtg tgc aat gac tat 199
 27 Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr
 W--> 28 40 45 50
 29 gct tca ggc tac cat tat gga gtc tgg tcc tgt gag ggc tgc aag gcc 247
 30 Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala
 W--> 31 55 60 65
 32 ttc ttc aag aga agt att caa gga cat aac gac tat atg tgt cca gcc 295
 33 Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala
 W--> 34 70 75 80 85
 35 acc aac cag tgc acc att gat aaa aac agg agg aag agc tgc cag gcc 343
 36 Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala
 W--> 37 90 95 100
 38 tgc cgg ctc cgt aaa tgc tac gaa gtg gga atg atg aaa ggt ggg ata 391
 39 Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile
 W--> 40 105 110 115
 41 cga aaa gac cga aga gga ggg aga atg ttg aaa cac aag cgc cag aga 439
 42 Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg
 W--> 43 120 125 130
 44 gat gat ggg gag ggc agg ggt gaa gtg ggg tct tga taatcaggtc 485
 45 Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser
 W--> 46 135 140 145
 47 agagtgacct gagctaaaat aacacattca gaattc 521
 49 <210> SEQ ID NO: 2

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Input Set : N:\Crif3\08132001\I486882.raw

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50 <211> LENGTH: 27
51 <212> TYPE: PRT
52 <213> ORGANISM: Recombinant human oestrogen
53 <400> SEQUENCE: 2
54     Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
55         1             5             10             15
56     Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln
57         20             25
59 <210> SEQ ID NO: 3
60 <211> LENGTH: 115
61 <212> TYPE: PRT
62 <213> ORGANISM: Recombinant human oestrogen
63 <400> SEQUENCE: 3
64     Ala Ala Ala Gly Gly Gly Gly Ser Met Glu Ser Ala Lys Glu Thr Arg
65         1             5             10             15
66     Tyr Cys Ala Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val
67         20             25             30
68     Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly
69         35             40             45
70     His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys
71         50             55             60
72     Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu
73         65             70             75             80
74     Val Gly Met Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg
75         85             90             95
76     Met Leu Lys His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu
77         100            105            110
78     Val Gly Ser
79         115
81 <210> SEQ ID NO: 4
82 <211> LENGTH: 102
83 <212> TYPE: DNA
84 <213> ORGANISM: human
85 <220> FEATURE:
86 <221> NAME/KEY: CDS
87 <222> LOCATION: (1)..(102)
88 <400> SEQUENCE: 4
89     aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat      48
90     Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
91         1             5             10             15
92     gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac      96
93     Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
94         20             25             30
95     ttc tat                                                                102
96     Phe Tyr
98 <210> SEQ ID NO: 5
99 <211> LENGTH: 34
100 <212> TYPE: PRT
101 <213> ORGANISM: human

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102 <400> SEQUENCE: 5
103   Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
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105   Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
106           20             25             30
107   Phe Tyr
109 <210> SEQ ID NO: 6
110 <211> LENGTH: 150
111 <212> TYPE: DNA
112 <213> ORGANISM: Human lymphocyte
113 <220> FEATURE:
114 <221> NAME/KEY: CDS
115 <222> LOCATION: (1)..(150)
116 <400> SEQUENCE: 6
117   atg gcc cag ccc acc acg cgt ccg ggc caa ggg aca cga ctg gac att   48
118   Met Ala Gln Pro Thr Thr Arg Pro Gly Gln Gly Thr Arg Leu Asp Ile
119       1             5             10             15
120   aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat   96
121   Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
122           20             25             30
123   gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac   144
124   Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
125           35             40             45
126   ttc tat   150
127   Phe Tyr
128       50
130 <210> SEQ ID NO: 7
131 <211> LENGTH: 50
132 <212> TYPE: PRT
133 <213> ORGANISM: Human lymphocyte
134 <400> SEQUENCE: 7
135   Met Ala Gln Pro Thr Thr Arg Pro Gly Gln Gly Thr Arg Leu Asp Ile
136       1             5             10             15
137   Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
138           20             25             30
139   Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
140           35             40             45
141   Phe Tyr
142       50
144 <210> SEQ ID NO: 8
145 <211> LENGTH: 150
146 <212> TYPE: DNA
147 <213> ORGANISM: Human lymphocyte
148 <220> FEATURE:
149 <221> NAME/KEY: CDS
150 <222> LOCATION: (1)..(150)
151 <400> SEQUENCE: 8
152   atg gcc cag tcc cac cac gcg tcc ggc gga ggg acc aag gtg gag atc   48
153   Met Ala Gln Ser His His Ala Ser Gly Gly Gly Thr Lys Val Glu Ile

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154      1      5      10      15
155    aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat 96
156    Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
157      20      25      30
158    gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac 144
159    Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
160      35      40      45
161    ttc tat 150
162    Phe Tyr
163      50
165 <210> SEQ ID NO: 9
166 <211> LENGTH: 50
167 <212> TYPE: PRT
168 <213> ORGANISM: Human lymphocyte
169 <400> SEQUENCE: 9
170    Met Ala Gln Ser His His Ala Ser Gly Gly Gly Thr Lys Val Glu Ile
171      1      5      10      15
172    Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
173      20      25      30
174    Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
175      35      40      45
176    Phe Tyr
177      50
179 <210> SEQ ID NO: 10
180 <211> LENGTH: 566
181 <212> TYPE: DNA
182 <213> ORGANISM: Recombinant human oestrogen
183 <220> FEATURE:
184 <221> NAME/KEY: CDS
185 <222> LOCATION: (41)..(475)
186 <400> SEQUENCE: 10
187    aagcttgcat gcaaaattcta tttcaaggag acagtcataa atg aaa tac cta ttg 55
188                                Met Lys Tyr Leu Leu
189                                1      5
190    cct acg gca gcc gct gga ttg tta tta ctc gcg gcc cag ccg gcc atg 103
191    Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met
192      10      15      20
193    gcc gag gtg caa ctg cag taa tag gcg gcc gca ggg gga gga ggg tcc 151
194    Ala Glu Val Gln Leu Gln Ala Ala Ala Gly Gly Gly Gly Ser
W--> 195      25      30      35
196    atg gaa tct gcc aag gag act cgc tac tgt gca gtg tgc aat gac tat 199
197    Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr
W--> 198      40      45      50
199    gct tca ggc tac cat tat gga gtc tgg tcc tgt gag ggc tgc aag gcc 247
200    Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala
W--> 201      55      60      65
202    ttc ttc aag aga agt att caa gga cat aac gac tat atg tgt cca gcc 295
203    Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala
W--> 204      70      75      80      85

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Output Set: N:\CRF3\09072001\I486882.raw

```

205      acc aac cag tgc acc att gat aaa aac agg agg aag agc tgc cag gcc      343
206      Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala
W--> 207      90      95      100
208      tgc cgg ctc cgt aaa tgc tac gaa gtg gga atg atg aaa ggt ggg ata      391
209      Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile
W--> 210      105      110      115
211      cga aaa gac cga aga gga ggg aga atg ttg aaa cac aag cgc cag aga      439
212      Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg
W--> 213      120      125      130
214      gat gat ggg gag ggc agg ggt gaa gtg ggg tct tga taatcaggtc      485
215      Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser
W--> 216      135      140      145
217      agagtgcacct gagctaaaat aacacattca ggtcgacttg ggtcagtcgt accggggacaa      545
218      agttaatgta acctcgaatt c      566
220 <210> SEQ ID NO: 11
221 <211> LENGTH: 27
222 <212> TYPE: PRT
223 <213> ORGANISM: Recombinant human oestrogen
224 <400> SEQUENCE: 11
225      Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
226      1      5      10      15
227      Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln
228      20      25
230 <210> SEQ ID NO: 12
231 <211> LENGTH: 115
232 <212> TYPE: PRT
233 <213> ORGANISM: Recombinant human oestrogen
234 <400> SEQUENCE: 12
235      Ala Ala Ala Gly Gly Gly Gly Ser Met Glu Ser Ala Lys Glu Thr Arg
236      1      5      10      15
237      Tyr Cys Ala Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val
238      20      25      30
239      Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly
240      35      40      45
241      His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys
242      50      55      60
243      Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu
244      65      70      75      80
245      Val Gly Met Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg
246      85      90      95
247      Met Leu Lys His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu
248      100      105      110
249      Val Gly Ser
250      115
252 <210> SEQ ID NO: 13
253 <211> LENGTH: 539
254 <212> TYPE: DNA
255 <213> ORGANISM: Recombinant human oestrogen
256 <220> FEATURE:

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FYI:

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

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TIME: 16:54:00

Input Set : N:\Crf3\08132001\I486882.raw

Output Set: N:\CRF3\09072001\I486882.raw

L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:25 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:28 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:31 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:37 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:450 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:450 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:450 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21